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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/836,470B

DATE: 02/21/2002
 TIME: 11:17:05

Input Set : A:\PTO.VSK.txt
 Output Set: N:\CRF3\02212002\I836470B.raw

ENTERED

3 <110> APPLICANT: KUWABARA, Yoko
 4 HASHIGUCHI, , Kenichi
 5 NAKAMATSU, Tsuyoshi
 6 KURAHASHI, Osamu
 7 MORI, Yukiko
 8 ITO, Hisao
 10 <120> TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM BACTERIA

AND METHOD FOR

11 PRODUCING L-ARGININE
 13 <130> FILE REFERENCE: 205801US0DIV
 15 <140> CURRENT APPLICATION NUMBER: US 09/836,470B
 16 <141> CURRENT FILING DATE: 2001-04-18
 18 <150> PRIOR APPLICATION NUMBER: US 09/629,616
 19 <151> PRIOR FILING DATE: 2000-07-31
 21 <150> PRIOR APPLICATION NUMBER: US 09/494,359
 22 <151> PRIOR FILING DATE: 2000-01-31
 24 <150> PRIOR APPLICATION NUMBER: JP 11-24149
 25 <151> PRIOR FILING DATE: 1999-02-01
 27 <160> NUMBER OF SEQ ID NOS: 7
 29 <170> SOFTWARE: PatentIn version 3.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 4837
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Brevibacterium lactofermentum
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (283)..(1461)
 39 <223> OTHER INFORMATION:
 42 <220> FEATURE:
 43 <221> NAME/KEY: CDS
 44 <222> LOCATION: (1470)..(4808)
 45 <223> OTHER INFORMATION:

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49 gatccaggaa aaacctggac agcatccggc cgcagactttg cgtccaaggc tgaaaacacc		120
51 ccatttgagg gccaggaatt cagcgctaag gtcacacaca ccgtgcttc tgccaagggtg		180
53 acttgtgcag acggagttgc gcaagacgc taacgggtgg gtgcata gtcacgcgcc		240
55 gcattgcata taatgcataa aattgaataa actacattca gggtatcaa ccagccaatt		294
57 tctttaaaaa agacagacac acgaaaggcg acaacagtca cc gtg agt aaa gac		
	Val Ser Lys Asp	
58	1	
59		
61 acc acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac		342
62 Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr		
63 5	10 15	20
65 ctg gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct		390

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66	Leu	Val	Leu	Ala	Asp	Gly	Arg	Thr	Phe	Thr	Gly	Phe	Gly	Phe	Gly	Ala
67																35
	25															
																30
69	atc	ggc	acc	acc	ctt	ggt	gag	gca	gtg	tcc	acc	acc	gcc	atg	acc	ggt
70	Ile	Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly
71																50
	40															45
73	tac	caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	gtt	gtg
74	Tyr	Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val
75																65
	55															60
77	gct	acc	gca	cca	cag	atc	ggt	aac	acc	ggc	tgg	aac	gat	gag	gac	aac
78	Ala	Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn
79																80
	70															75
81	gag	tcc	cgc	gac	ggc	aag	att	tgg	gtt	gca	ggc	ctt	gtt	atc	cgc	gac
82	Glu	Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp
83																100
	85															95
85	ctc	gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag
86	Leu	Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln
87																115
	105															110
89	gaa	atg	gca	gac	caa	ggc	atc	gtc	ggc	atc	ggc	gga	atc	gac	acc	cgc
90	Glu	Met	Ala	Asp	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg
91																130
	120															125
93	gca	ctg	gtt	cgc	cac	ctg	cgc	aac	gaa	ggt	tcc	atc	gca	gcg	ggc	atc
94	Ala	Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Gly	Ile	
95																145
	135															140
97	ttc	tcc	ggc	gct	gac	gca	cag	cgc	cca	gtt	gaa	gaa	ctc	gtt	gag	atc
98	Phe	Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile
99																160
	150															155
101	gtc	aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc
102	Val	Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val
103																170
	165															175
105	tct	gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gag	ggc	gaa	gag	cgc	cac
106	Ser	Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His
107																195
	185															190
109	acc	gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt
110	Thr	Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg
111																200
	200															205
113	ttc	tct	gca	cgc	ggt	gtt	cgc	acc	gtc	atc	gtc	cct	gct	gaa	acc	cca
114	Phe	Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro
115																220
	215															225
117	ttg	gag	gac	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttt	atc	tcc	aat
118	Leu	Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn
119																235
	230															240
121	ggc	cct	ggc	gac	cct	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	
122	Gly	Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg
123																250
	245															255
125	gaa	gtt	ctg	gaa	gcc	gac	att	cca	tcc	ttt	ggc	atc	tgc	tcc	ggc	aac
126	Glu	Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn
127																265
	265															270
129	cag	atc	ctc	ggc	cgc	gca	tcc	ggc	atg	gag	acc	tac	aag	ctg	aag	tcc
130	Gln	Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	Lys	Leu	Lys	Phe

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133	ggc cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag			1206
134	Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys			
135	295	300	305	
137	atc gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca			1254
138	Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala			
139	310	315	320	
141	ggc cag gaa ttc gag aca gat ttc ggc act gcg att gtc acc cac acc			1302
142	Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr			
143	325	330	335	340
145	tgc ctt aac gac ggc gtc gtt gaa ggt gtt gcg ctg aag tcc gga cgc			1350
146	Cys Leu Asn Asp Gly Val Val Glu Gly Val Ala Leu Lys Ser Gly Arg			
147	345	350	355	
149	gca tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat			1398
150	Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Gly Pro Asn Asp			
151	360	365	370	
153	gca agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct			1446
154	Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala			
155	375	380	385	
157	cag aag aaa ggc gca taaataac atg cca aag cgt tca gat att aac cac			1496
158	Gln Lys Lys Gly Ala Met Pro Lys Arg Ser Asp Ile Asn His			
159	390	395	400	
161	gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc cag gca tgt gaa			1544
162	Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly Gln Ala Cys Glu			
163	405	410	415	
165	ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg aag gaa gag gga			1592
166	Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu Lys Glu Glu Gly			
167	420	425	430	
169	ctg cgc gtc acc ctc atc aac tcc aac cca gca acg atc atg acc gac			1640
170	Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr Ile Met Thr Asp			
171	435	440	445	450
173	cca gaa atg gct gac cac acc tac gtg gag cca atc gag ccg gaa tac			1688
174	Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr			
175	455	460	465	
177	atc gac aag att ttc gct aag gag atc gag cag ggc cac cca atc gac			1736
178	Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly His Pro Ile Asp			
179	470	475	480	
181	gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt aac gca gct atc			1784
182	Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile			
183	485	490	495	
185	cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc gtt gaa ctc atc			1832
186	Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile			
187	500	505	510	
189	ggt gca gac atc gat gcc att gag cgc ggc gaa gat cgc cag aag ttc			1880
190	Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe			
191	515	520	525	530
193	aag gat att gtc acc acc atc ggt ggc gaa tcc gcg cgt tcc cgc gtc			1928
194	Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala Arg Ser Arg Val			
195	535	540	545	

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197 tgc cac aac atg gac gaa gtc cat gag act gtc gca gaa ctt ggc ctt	1976
198 Cys His Asn Met Asp Glu Val His Glu Thr Val Ala Glu Leu Gly Leu	
199 550 555 560	
201 cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc ctg ggc tcc ggt	2024
202 Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly Leu Gly Ser Gly	
203 565 570 575	
205 ctt gca tac aac acc gaa gac ctt gag cgc atc gca ggt ggc gga ctt	2072
206 Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu	
207 580 585 590	
209 gct gca tct cct gaa gca aac gtc ttg atc gaa gaa tcc atc ctt ggt	2120
210 Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Ser Ile Leu Gly	
211 595 600 605 610	
213 tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc gca gac aac gtt	2168
214 Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr Ala Asp Asn Val	
215 615 620 625	
217 gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg ggc gtg cac acc	2216
218 Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu Gly Val His Thr	
219 630 635 640	
221 ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg act gac cgt gaa	2264
222 Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu	
223 645 650 655	
225 ttc cag aag atg cgc gat cag ggt atc gcc atc atc cgc gag gtc ggc	2312
226 Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Arg Glu Val Gly	
227 660 665 670	
229 gtg gac acc ggt gga tgt aac atc cag ttc gct atc aac cca gtt gat	2360
230 Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile Asn Pro Val Asp	
231 675 680 685 690	
233 ggc cgc atc atc acc att gag atg aac cca cgt gtg tct cgt tcc tcc	2408
234 Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val Ser Arg Ser Ser	
235 695 700 705	
237 gcg ctg gca tcc aag gca acg ggc ttc cca att gcc aag atg gct gcc	2456
238 Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala Lys Met Ala Ala	
239 710 715 720	
241 aag ctg gct atc gga tac acc ctg gat gag atc acc aac gac atc act	2504
242 Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr	
243 725 730 735	
245 ggt gaa acc cca gct gcg ttt gag ccc acc atc gac tac gtc gtg gtc	2552
246 Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp Tyr Val Val Val	
247 740 745 750	
249 aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc gct gat gac act	2600
250 Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly Ala Asp Asp Thr	
251 755 760 765 770	
253 ttg acc acc acc atg aag tcc gtc ggt gag gtc atg tcc ctg ggc cgt	2648
254 Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met Ser Leu Gly Arg	
255 775 780 785	
257 aac tac att gca gca ctg aac aag gca ctg cgt tcc ctg gaa acc aag	2696
258 Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys	
259 790 795 800	
261 cag cag ggt ttc tgg acc aag cct gat gag ttc ttc gca ggg gag cgc	2744

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262 Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg		
263 805 810 815		
265 gct acc gat aag gca gct gtt ctg gaa gat ctc aag cgc cca acc gaa	2792	
266 Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys Arg Pro Thr Glu		
267 820 825 830		
269 ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt ggc gca agc gtg	2840	
270 Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu Gly Ala Ser Val		
271 835 840 845 850		
273 gaa gaa ctc tac gaa gca tct tct att gat cct tgg ttc ctc gcc gag	2888	
274 Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu		
275 855 860 865		
277 ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt gac gca cca ttc	2936	
278 Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val Asp Ala Pro Phe		
279 870 875 880		
281 ctc aac gaa gat ctc ctg cgc gaa gca aag ttc atg ggt ctg tcc gac	2984	
282 Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met Gly Leu Ser Asp		
283 885 890 895		
285 ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc gaa gac ggc gta	3032	
286 Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly Glu Asp Gly Val		
287 900 905 910		
289 cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta ttc aag act gtg	3080	
290 Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val Phe Lys Thr Val		
291 915 920 925 930		
293 gat acc tgt gca gca gag ttt gaa gct aag act ccg tac cac tac tcc	3128	
294 Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser		
295 935 940 945		
297 gca tac gag ctg gat cca gca gct gag tct gag gtc gca cca cag act	3176	
298 Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val Ala Pro Gln Thr		
299 950 955 960		
301 gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca aac cgc atc ggc	3224	
302 Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly		
303 965 970 975		
305 cag ggc atc gag ttc gac tat tcc tgt gtt cac gca gct ctt gag ctc	3272	
306 Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala Ala Leu Glu Leu		
307 980 985 990		
309 tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc aac cca gag	3317	
310 Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys Asn Pro Glu		
311 995 1000 1005		
313 acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac ttc gag	3362	
314 Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr Phe Glu		
315 1010 1015 1020		
317 cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag gcg	3407	
318 Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu Ala		
319 1025 1030 1035		
321 cag tcc ggc acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag	3452	
322 Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln		
323 1040 1045 1050		
325 act cct ctg ggc ttg gca gat cgt ttg aag aag gct ggc gtc cct	3497	
326 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro		

VERIFICATION SUMMARY

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